

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/553,305
Source: PT/10
Date Processed by STIC: 10/25/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>, **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/553,305

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 10/25/2005

PATENT APPLICATION: US/10/553,305

TIME: 10:08:24

Input Set : A:\sequence_listing.txt

Output Set: N:\CRF4\10252005\J553305.raw

3 <110> APPLICANT: Japan EnviroChemicals, Ltd.
 5 <120> TITLE OF INVENTION: A protein binding to plasticizers
 7 <130> FILE REFERENCE: 09622
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,305
 C--> 9 <141> CURRENT FILING DATE: 2005-10-14
 9 <150> PRIOR APPLICATION NUMBER: JP 2003-110877
 W--> 10 <151> PRIOR FILING DATE: (2003-4-15) 2003-04-15 ← use this format for dates
 E--> 12 <160> NUMBER OF SEQ ID NOS: (27) 34 ← see p. 2
 14 <170> SOFTWARE: PatentIn version 3.1

pp 1-4

ERRORED SEQUENCES

155 <210> SEQ ID NO: 5
 156 <211> LENGTH: (5) 15 shown below
 157 <212> TYPE: PRI
 158 <213> ORGANISM: Artificial
 160 <220> FEATURE:
 161 <223> OTHER INFORMATION: (Linker)
 163 <400> SEQUENCE: 5
 164 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 E--> 165 1 5 10 15
 273 <210> SEQ ID NO: 15
 274 <211> LENGTH: (20) 36 (p. 2)
 275 <212> TYPE: DNA
 276 <213> ORGANISM: Artificial
 278 <220> FEATURE:
 279 <223> OTHER INFORMATION: Primer
 281 <220> FEATURE:
 282 <221> NAME/KEY: misc_feature
 283 <222> LOCATION: 24
 284 <223> OTHER INFORMATION: i
 286 <220> FEATURE:
 287 <221> NAME/KEY: misc_feature
 288 <222> LOCATION: 25
 289 <223> OTHER INFORMATION: i
 291 <220> FEATURE:
 292 <221> NAME/KEY: misc_feature
 293 <222> LOCATION: 29
 294 <223> OTHER INFORMATION: i
 296 <220> FEATURE:
 297 <221> NAME/KEY: misc_feature
 298 <222> LOCATION: 30

Does Not Comply
Corrected Diskette Needed

what is the source of genetic material?

(see item 11 on

Envr

summary

sheet)

Please
correct this
in subsequent
sequences

P. 2

RAW SEQUENCE LISTING

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Input Set : A:\sequence_listing.txt

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299 <223> OTHER INFORMATION: i /
 301 <220> FEATURE:
 302 <221> NAME/KEY: misc_feature
 303 <222> LOCATION: 34
 304 <223> OTHER INFORMATION: i /
 306 <220> FEATURE:
 307 <221> NAME/KEY: misc_feature
 308 <222> LOCATION: 35 /
 309 <223> OTHER INFORMATION: i
 311 <400> SEQUENCE: 15
 E--> 312 ggccacgcgt cgactagtagt ggg^hhggg^hnnn ggg^hnn^hg
 612 <210> SEQ ID NO: 34 ← last sequence in submitted file
 613 <211> LENGTH: 66
 614 <212> TYPE: PRT
 615 <213> ORGANISM: Artificial → S shown below
 617 <220> FEATURE:
 618 <223> OTHER INFORMATION: Primer
 620 <400> SEQUENCE: 34
 621 Gly Gly Gly Gly Ser
 E--> 622 1 5

36

a primer is not a peptide
 (please give source of genetic material
 as explanation)

10/553,305

3

<210> 10

<211> 18

<212> DNA

<213> Artificial

needs explanation

(see p. 4)

<400> 10

gcttgccggg tgggccac

for

error explanation

4

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/553,305

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TIME: 10:08:25

Input Set : A:\sequence_listing.txt
Output Set: N:\CRF4\10252005\J553305.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,28,29,30,31,32,33,34

Use of <220> Feature(NEW RULES): *error explanation*

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:10

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/553,305

DATE: 10/25/2005

TIME: 10:08:25

Input Set : A:\sequence_listing.txt

Output Set: N:\CRF4\10252005\J553305.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24
L:99 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:97
L:165 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:15 SEQ:5
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:226 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:226 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:226
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:312 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:36 SEQ:15
L:622 M:252 E: No. of Seq. differs, <211> LENGTH:Input:66 Found:5 SEQ:34
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (27) Counted (34)